

acc taa gac agc gga cca gac ggc acc cca gac acc gtc tac agc atc Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile 40 45 50 55	198
gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys 60 65 70	246
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acc ggc aac Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn 75 80 85	294
ctc acg gag ctc tac tat gcc agg gtc acc gct gtc aat gag gga ggc Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly 90 95 100	342
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr 105 110 115	390
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tgg att Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile 120 125 130 135	438
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly 140 145 150	486
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu 155 160 165	534
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gaa ggc aag cag Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln 170 175 180	582
aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly 185 190 195	630
acc atc ata att tgc gtt ccc acc tga acc aac aac att acc tcc tac 200 205 210 215 220 225	678

Thr Thr Met Thr Val Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr	200	205	210	215	
atg tac cca att cca acc cta cca acc cca acc cca acc cca acc cca acc	Met Lys Arg Val Gly Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	220	225	230	235
ttc gga acc ttc cta ttc ttc atg gaa ttc cta atc gaa gta cta cta	Ser Gly Ala Thr Leu Pro Ser Met Gly Phe Leu Val Ala Val Leu Tyr	235	240	245	250
tac cta acc tca acc tat gta acc gaa cca cta gaa cca cta gaa cta	Tyr Leu Ser Tyr Arg Tyr Val Thr Trp Trp Pro Ala Pro Trp Asn Ser	255	260	265	270
ctg aac atc caa caa atc ctg act ttc caa cca ctg gaa ttc atc caa	Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	265	270	275	280
gag cac atc cta atc cct gtc ttt gac ctc agc ggc ccc aac aat ctg	Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	280	285	290	295
gcc caa cct gtc caa tac tcc caa atc aag ctg tct gga ccc aag gaa	Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	300	305	310	315
ccc gca gga gct cca caa cga cat aac ctg tcc gag atc acc tac tta	Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	315	320	325	330
ggg caa cca gaa acc ttc atc ctc caa ccc tcc aac gta cca act ccc	Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	330	335	340	345
cag atc ctc tcc cca cta tcc tat gaa cca aac gct acc ctt gaa atc	Gln Ile Leu Ser Pro Leu Ser Trp Ala Pro Asn Ala Ala Pro Gln Val	345	350	355	360
gag ccc cca acc tca acc ttc cca acc cca gaa gct cca ttc cca	Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	365	370	375	380

ttt tac ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	1276
Pro Tyr Ala Pro Gln Ala Thr Ser Tyr Val Gln Pro Ser Ser Tyr Ala	
395 396 397	
ccg caa ccc act cca caa caa tgg ctt cca tcc tat agg gta tgc ata	1284
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
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Glu Gly Ser Gly Tyr Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Tyr	
410 415 420	
cac ctt agg cct aat aat gag ctt cag aaa aag cca cca act gga aac	1350
His Leu Arg Pro Tyr Gly Gln Leu Gln Tyr Glu Pro Pro Ala Gly Ser	
425 430 435	
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Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
440 445 450 455	
gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc	1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
460 465 470	
aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
475 480 485	
aca cca cag tac cta aag ggc cag ctg ccc ctg ctg tcc tca gtc cag	1542
Thr Pro Gln Tyr Leu Tyr Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
490 495 500	
atc gag ggc cac ccc atg tcc ctg cct ttg caa cct cct tcc ggt cca	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
505 510 515	
tgt tcc ccc tca gaa caa aat cca aat ccc tga ggc ctg ctg gaa tcc	1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
520 525 530 535	
ctt gta tat ttt aat aat aat aat aat aat aat aat aat aat aat aat	1686
Leu Val Tyr Thr Thr Asp Glu Ala Lys Ser Pro Ala Pro Gln Thr Ser	
540 545 550	

gac cta gaa cag ttc tta tta tta gat tat ttt ttt tta gac ctg gaa 1764
 Asp Leu Glu Gln Pro Thr Ala Leu Asp Ser Leu Thr Arg Gly Leu Ala
 555 560 565

ctg act gtg cag tgg gaa ttc tgaaggggaat gggaaaagact tgaatgattac 1785
 Leu Thr Val Gln Trp Glu Ser
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tccctatccc taaccagtat caccatcttg gctgtcaatc ccattgctgc ccattgccaac 1845
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<213> Homo sapien

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 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60

401 Ser Thr Ala Val Val Met Thr Gly Ser Thr Val Arg Ser Pro Thr
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Ser Ser Leu Glu Met His Thr Ser Val Pro Pro Asp Val Thr Tyr 110
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 Ser Lys Val Arg Ser Ile Glu Met Ile Val His Pro Thr Pro Thr Pro
 His 120 125
 Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
 130 135 140
 Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
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 Thr Trp Thr
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<212> PRI

<213> Artificial Sequence

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<212> PRI

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acccctgagg tcacatggt ggtggtggac gtgagccag aagacccga ggtcaagtt	180
aactggtacg tggacggtt ggaggtgat aatgcaga caaagccgca ggaggaagag	240
tacaacagca cttacgtgt ggtcaggtc ctcacgttc tgcacagga ctggtgaat	300
ggcaggagt ac aagtgc aa ggtctcaac aaagccctc cctctcat cgaqaaaac	360
ttctcaaaq caaaggga gccccgagaa ccacaggtt acacctgac cccatccgg	420
gatgagtga caaagaaca ggtcaggtt acctgctgg tcaaggttt ctatccagc	480
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cccgtgttg actccaggg ctcttcttc ctctacagca agctacgt ggacaagagc	600
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ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg	101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu	
15 20 25	
gta cag gca gga gca gct ggg ccc atc agc tcc cag tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	
agg tcc aac ttc ttc ttc ctt tat atc aac cgc acc ttc atc tgc	197

Lys Ser Asn Phe Glu Gln Pro Tyr Ile Thr Asp Arg Thr Phe Met Leu
45 50 55

gct aag gag gct aac tta gct cat aac aac aca gac att cgt ctc att 245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
60 65 70 75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
80 85 90

atg aag cag gtg ctg aac ttc aac ctt gaa gaa gtg ctg ttc cct caa 341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
95 100 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
110 115 120

agg ctg agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
125 130 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140 145 150 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
160 165 170

atg tct ctg aga aat acc tgc att tgaccagagc aaagctgaaa aatgaataac 567
Met Ser Leu Arg Asn Ala Cys Ile
175

aaacccctt tccctgctag aaataacaat tagatcccc aaagcattt ttitttaacca 647
aaaggaagat gggagacaaa actccatcat gatggatgga ttccaaatga acccctgngt 707
taattacaaa ggaacacaaat gccacttttg ttataagac tagaaggtag attttctaac 767
catagatatt tattgataac atttcattgt aactggtatt ctatacacaq aaaacaattt 827
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tattattata aaactgcatt ttatttatat catittatit atatgualit atttataqaa 1007
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1116

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<213> homo sapiens

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Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
 20          25          30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35          40          45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50          55          60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65          70          75          80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85          90          95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
100          105          110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
115          120          125
Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
130          135          140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145          150          155          160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
165          170          175
Ala Cys Ile

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<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer 1928-90

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His His His His His His

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5

<210> 14

<211> 63

<212> DNA

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63

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<212> DNA

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<212> Other nucleotide primer (5' to 3')

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cagtgaatc cgaagggaac gtttcgtc

28

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<212> DNA

<213> Homo sapiens

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<222> (1) ... (660)

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48

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

96

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

144

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

192

aaa tat atg aat act acc ttg aca gaa tat gat ttc tca aat ctt tcc
Lys Gln Met Asp Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

240

aag tat aat aac cac acc ttg aca gtc aag act gaa ttt gca gat gaa
Lys Tyr Glu Asp His Thr Leu Asn Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

288

cat tgc att ttt cta ggc att tgc ttt ttt ttt ttt ttt ttt ttt ttt

336

Pro Ser Arg Thr Val Arg Ile Thr Glu Val Pro Val Asp Asp Thr Thr
100 105 110

att gga ccc cct gaa atg caa ata gaa gta ctt gat gat tct tta cat 384
Ile Gly Pro Pro Gly Met Gln Val Ala Val Leu Asp Asp Ser Thr His
115 120 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
195 200 205

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Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
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<213> Homo sapiens

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 Asn Leu Thr Phe Thr Ala Val Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
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 Lys Lys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
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 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
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 Ile Gly Pro Pro Gly Met Val Val Glu Val Leu Asp Asp Ser Leu His
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 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
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 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
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 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
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 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
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 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
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<212> DNA

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<223> Oligonucleotide primer AC38931

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acaaagccac ggaaggaag

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<212> DNA

<213> Artificial Sequence

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<23> Oligo nucleotide primer (5' end)

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gtttactcgg agacaggag ag 82

<10> 22

<11> 1428

<12> DNA

<13> Artificial Sequence

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<21> CDS

<22> (1)...(1428)

<23> CRF2-4 extracellular cytokine binding domain fused
to IgG1 with a 6-HIS tag

<400> 22

atg ggg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

aaa tgc atg aat act acc ttg acg gaa tat gat ttc tca aat ctt tcc 240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

aag tat gat gac cgc acc tta aga gtc aag gct gaa ttt gca gat gag 288
Lys Tyr Glu Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

cat tca gac tga cta tca tta ttc tgt ctt tta tat gac acc att Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile 100 105 110	336
att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His 115 120 125	384
atg cgt ttc tta ggc cct aaa att gaa aat gaa tac gaa act tgg act Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr 130 135 140	432
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys 145 150 155 160	480
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu 165 170 175	528
gtc ctc aga aac ctg gag cca tgg aca act tat tgt qtt caa gtt cga Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg 180 185 190	576
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val 195 200 205	624
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tgg Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser 210 215 220	672
ggt tgg ggt tgg gag ccc aca tca tca gac aaa act cac aca tgc cca Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro 225 230 235 240	720
ccg tgc cca gca cct gaa gct gaa ggg gca ccc tca atc ttc ctc ttc Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe 245 250 255	768
ccc cca aaa ccc aag gaa acg ctc ata atc tcc cga acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Ser Thr Pro Glu Val 260 265 270	816

aca tac gta ata ata gac atg aac val aaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 275 280 285	364
aac tgg tac gta gac ggc gtg gag gta cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 290 295 300	312
cgg gag gag cag tac aac aac aac tac cgt gta gtc agc gtc ctc aac Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr 305 310 315 320	360
gtc ctg cac cag gac taa cta aat gcc aag gag tac aag ttc aag gtc Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val 325 330 335	1008
tcg aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala 340 345 350	1056
aaa ggg cag ccc cga gaa cca cag gta tac acc ctg ccc cca tac cgg Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg 355 360 365	1104
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa gcc Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly 370 375 380	1152
ttc tat ccc acc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro 385 390 395 400	1200
cag aac aac tac aag acc agc cct ccc atg ctg gac tcc gac ggc tcc Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser 405 410 415	1248
ttc ttc ctc tac aac aag ctg acc atg aac aag aac agg tgg cag cag Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 420 425 430	1296
aaa aac atc atc tca tgc tcc gta ata atc aac cct cta cac aac aac	1344

Gly Asn val Phe Ser Ser Val Met His Glu Ala Leu His Asn His
435 440 445

tac acg caa aag aac etc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt 1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
450 455 460

ggt tcc gga tca ggt aac cat cac cat cac cat cac 1418
Gly Ser Gly Ser Gly Gly His His His His His His
465 470 475

<210> 23

<211> 476

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15
Ala Leu Gly Met val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
115 120 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
130 135 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145 150 155 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
165 170 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
180 185 190

<220>

<223> Oligonucleotide primer ZC29328

<400> 24

tcaggggat cggtttcgg ttccgggttc gaggc aat catcagacaa aactcaaca 60
tgc 63

<210> 25

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29231

<400> 25

gaactgactc gagctactcc ataggeatat actgccacc tgatcctta cccggagaca 60
gggag 65

<210> 26

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39335

<400> 26

atcqaattc gcaagcca tgaggacgt gctgaccatc ttgactgtgg ggtccctggc 60
tcttaccgc 70

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC28981

<400> 27

tttgggc tctttat tctgtgaa 26

<210> 28

<211> =

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer 7039043

<400> 28

ctgactcgaq ctactccata ggcataatact cggcacctga tctggaacaa cgcggaacca 60
gtttacccaa agacaggag 80

<210> 29

<211> 1457

<212> DNA

<213> Artificial Sequence

<220>

<223> hcytoril extracellular cytokine binding domain
fused to IgG1 with a Glu-Glu tag

<221> CDS

<222> (1)...(1452)

<400> 29

atg aag aag ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac 48
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
1 5 10 15

gcc cct gaq gac ccc tgg gat ctg ctc cag cac gtg aaa ttc cag tcc 96
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
20 25 30

agg aac ttt gaa aac atc cta aag tgg gac agc ggg cca gag ggc acc 144
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
35 40 45

cca gac aca atc tac aac atc gaa tat aag aag tac gaa gaa aag aac 192
Pro Asp Thr Val Lys Ser His Glu Lys Lys Thr Lys Gly Glu Arg Asp
50 55 60

tgg gta tca aag aag ggc tat aag aag ata acc cag aag tcc tac aac 240
Trp Val Ala Lys Lys Gly Lys Glu Arg Ile Thr Arg Lys Ser Lys Asn
65 70 75

ctg acc ata aat aat gaa aac ttc ttc ttc ttc tac tat gac agc att Leu Thr Val Glu Leu Gly Asn Leu Thr Val Leu Lys Lys Ala Arg Val 80 90 95	288
acc gct gtc aat gag gga ggc cgg tca acc acc aag atg act gac aag Ile Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg 100 105 110	336
ttc agc tct cta cag cac act acc ctc aag cca cct gat gtg acc tat Phe Ser Ser Leu Glu His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys 115 120 125	384
atc tcc aaa gtg aua tcg att cag atc att gtt cat cct acc ccc aag Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr 130 135 140	432
cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe 145 150 155 160	480
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln 165 170 175	528
atg cac ctt gga qqq aag cag aga gaa tat gag ttc ttc ggc ctg acc Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr 180 185 190	576
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp 195 200 205	624
ggc aag gag aat aat ccc tac atg tgc caa gtg aag aca ctg cca gac Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp 210 215 220	672
cgg aca taa acc aca tcc ggt tcg ggt tca ggt tcg gag ccc aca tca Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser 225 230 235 240	720
tca gac aaa act ttc aca tgc caa ttc ttc ttc aca cct gaa ggc aag 245 250 255 260	768

cca atg cta gac tca aac aca tca ttc ttc ctc tca aca aac tca acc 1396
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430

gta gac aag agc agg tag caa caa gag aac gtc ttc tca tgc tcc gta 1344
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

atg cat gag gct ctg cac aac cac tac aag cag aag agc ctc tcc ctg 1392
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat 1440
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480

atg cct atg gag 1452
 Met Pro Met Glu

<210> 30

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide encoded by the hzcytor11 extracellular
 cytokine binding domain fused to IgGg1 with a
 Glu Glu tag of SEQ ID NO: 29

<400> 30

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1 5 10 15
 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80

Leu Thr Val Ala Thr Gly Asn Leu Thr Ala Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
 225 230 235 240
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 245 250 255
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415

Pro Val Leu Asp Ser Arg Gly Ser Phe Thr Ser Tyr Ser Lys Leu Thr
 420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480

Met Pro Met Glu

<10> 31

<11> 22

<12> DNA

<13> Artificial Sequence

<20>

<23> Oligonucleotide primer ZC37693

<400> 31

ctccagacac ggtctacagc at

22

<10> 32

<11> 23

<12> DNA

<13> Artificial Sequence

<20>

<23> Oligonucleotide primer ZC37449

<400> 32

gggtcagccc gaagaactca tat

23

<210> 33

<211> 199

<212> PR1

<213> Homo sapiens

<400> 33

Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
 1 5 10 15

Asn Ile Leu Glu Trp Glu Ser Ser Ala Thr Ala Lys Glu Asn Leu Thr
 1 5 10 15 20 25 30
 Phe Thr Ala Glu Tyr Leu Ser Tyr Arg Thr Phe Glu Asp Lys Lys Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Glu Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Glu Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Glu Ile Thr Pro Glu Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Glu Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Glu
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

s210> 34
 s211> 211
 s212> PRI
 s213> Homo sapiens

s400> 34
 Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
 1 5 10 15
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
 20 25 30
 Glu Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Glu Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80

Arg Val Arg Ala Val Arg Val Ser Arg His Ser Asn Trp Thr Val Thr
 95
 Asn Thr Arg Phe Ser Val Arg Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
 Thr Arg Gln
 210

<210> 35

<211> 201

<212> PRT

<213> Homo sapiens

<400> 35

Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 1 5 10 15
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
 20 25 30
 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 35 40 45
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 50 55 60
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
 65 70 75 80
 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
 85 90 95
 Ile Leu Lys His Leu Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 100 105 110
 Gly Met Glu Ile Thr Lys Asp Gly Phe Leu Leu Val Ile Glu Leu Glu
 115 120 125

Arg Ser Gly Phe Thr Ser Gly Pro Leu Val Ala Tyr Asp Arg Arg Glu
135 140 145

Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145 150 155 160

Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
165 170 175

Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
180 185 190

Glu Lys Val Glu Val Gln Gly Ala Ala
195 200